

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model
 Run on: March 15, 2003, 15:07:49 ; Search time 74.0238 Seconds
 (without alignments)
 1537.035 Million cell updates/sec

Title: US-08-978-217-2
 Perfect score: 1980

Sequence: 1 MAATCEISNIFNSYFSAMYS..... YKFGKNSSGKEREVLOSRN 371

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapekt 0.5
 Ygapop 10.0 , Ygapekt 0.5
 Fgapop 6.0 , Fgapekt 7.0
 Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFM=fastap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=5its -START=1 -END=-1 -MATRIXX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLON=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=psq -NORM=ext -HEAPSIZE=5000 -MILEN=0 -MAXLEN=2000000000
-USER=US08978217 @CGN 1_1_131 @runat 1402003_141838_13457 -NCPU=5 -ICU=3
-NO_XLKY -NO_MMTP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADD=1 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

Issued Patents NA:*

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 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PC7US_Comb.seq:*
 6: /cgn2_6/ptodata/1/ina/backfile1.seq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description	ALIGNMENTS
1	1980	100.0	1920	1 US-08-746-789A-1	Sequence 1, Appli	Sequence 6, Appli
2	559	28.2	5427	3 US-09-009-913-2	Sequence 2, Appli	Sequence 10, Appli
3	555.5	28.1	5510	3 US-09-009-913-3	Sequence 3, Appli	Sequence 1, Appli
4	555.5	28.1	5667	3 US-09-009-913-4	Sequence 4, Appli	Sequence 3, Appli
5	519.5	26.2	852	4 US-09-020-956-44	Sequence 44, Appli	Sequence 2, Appli
6	519.5	26.2	852	4 US-09-030-607-44	Sequence 44, Appli	Sequence 1, Appli
7	519.5	26.2	852	4 US-09-605-785-44	Sequence 44, Appli	Sequence 1, Appli
8	519.5	26.2	852	4 US-03-439-313-44	Sequence 44, Appli	Sequence 43, Appli
9	519.5	26.2	852	4 US-09-352-616A-44	Sequence 44, Appli	Sequence 9, Appli
10	519.5	26.2	852	4 US-09-232-149A-44	Sequence 44, Appli	Sequence 3, Appli
11	486.5	24.6	848	3 US-09-009-913-338	Sequence 338, Appli	Sequence 3, Appli
12	422	21.3	2280	3 US-09-009-913-8	Sequence 8, Appli	Sequence 2, Appli

QY 27 AlaSerValProProAlaAlaThr-----PheGlyAlaAspLeuValLeuThr 43
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 Db 84 GCTGCCCTCCCTCCATCACGCCACAGCTATTCCACCCAGATCTTGTAGGA--- 140
 QY 44 LeuSerAsnProGlnMetSerLeuGluGly----- 53
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 Db 141 -----ARTGAGATCATGATCTGGAAAGGGTGTAAATGATTCACCCGGCAAC 194
 QY 54 -----ThrglyuLysLeuGlu----- 58
 ||||: : ||||: : ||||: : ||||: : ||||: : ||||: :
 Db 195 AACCTCTTCACCAGGCCAGCCTGACAGCTACTCCACGTCATGTCAAATGTTTCAGT 254
 QY 59 -----TripleuGlyGluGlnProGlnPheTpSerLysThrGlnVal 72
 ||||: : ||||: : ||||: : ||||: : ||||: : ||||: :
 Db 255 GGTTTCTTGAGGCAGTGGCAATTCTCATCCCTAGTAGCTGACCAAGTACGGGTG 314
 QY 73 LeuAspTrpIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerAlaLeuPhe 92
 ||||: : ||||: : ||||: : ||||: : ||||: : ||||: : ||||: :
 Db 315 TCGGAGTGGCTCAGACCTCTGGACACCACCGCTGGATGCCAATGATCCCTTC 374
 QY 93 SerArgCysAsnMetAspGlyAlaLysLeuCysAbnCysAlaLeuGluGluLeu 112
 ||||: : ||||: : ||||: : ||||: : ||||: : ||||: : ||||: :
 Db 375 CAGTAGCTGACATCACGGCAGACCTCTGGCTGAGTGTGGAGGTCACCCGG 434
 QY 113 ValPheGlyProLeuGlyAspGlnLeuLeuAlaGluLeuAspLeuThr----- 129
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 Db 435 GGGGCGGGACCGCGGGCAGTCCCTACAGCAACTGCACTCTGAAAGGGACGGC 494
 QY 130 SerSerSerSerAspGluLeuSerTrpIleLeuGluLeuLeuGluLysAspGlyMta 149
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 Db 495 CAGTGCGTAGTGAC----- 512
 QY 150 PheGlyIgluAlaLeuAspProGlyProPheAspGlyIleSerProPheAlaGlnGluLeu 169
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 Db 513 TCCCCATGCC----- 533
 QY 170 LeuAspAspGlyGlnGlnAlaSerPheTpSerLysGlyAlaGlyAlaPro 189
 ::: ||||: : ||||: : ||||: : ||||: : ||||: :
 Db 534 ATGGTCAGACTGAAACAATGAGCCCT----- 560
 QY 190 SerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerHisSer 209
 ||||: : ||||: : ||||: : ||||: : ||||: :
 Db 561 -----TCCATCATGAAACACTCTGAAGAACGAGAACTTAT 599
 QY 210 SerAspSerGlySerAspTyrAlaAspLeuAspProThrAspGlyLysLeuPheProSer 229
 ||||: : ||||: : ||||: : ||||: : ||||: : ||||: :
 Db 600 GACACCACTCTGGTACAGCTGAGATG-----TGGACAGCAACTTC----- 647
 QY 230 AspGlyPheArgAspCysLys----- 237
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 Db 648 -----TCCGGGTCATCTCCATGACAACACCACTCACCTTCCTGTT 692
 QY 238 GlyAspProLysHistidylLysArgLysArgLysArgLysLeuSerLysGluTyr 257
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 Db 693 GCGAGTCACCTGATATGAAAGGAGCAAGCCCCCTGCCAACACCAAN--- 749
 QY 258 TrpAspCysIleGluGlyLysLysSerLysHisAlaProArgLysTyrHisLeuPheGlu 277
 ||||: : ||||: : ||||: : ||||: : ||||: : ||||: :
 Db 750 -----AAGCAACCCGAGGAGCTACATGAA 782
 QY 278 PhelIeArgAspIleLeuLeuHisProGluLeuLysGluGlyLeuMetLysTpGluAsn 297
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 QY 298 ArgHisGluGlyValPheLysLysSerLysHisAlaProArgLysTyrHisLeuPheGlu 317
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 Db 843 CGATCTGAGGGCTCTCAGGTCTGAAATCAGGGAGCTACATGGTAA 902
 QY 318 LysLysLysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrTyr 337
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 Db 903 ArgGAGGAGAACAGCAGCAGCTGATGAAAGCTCAGCCGAGCTATGAGATATTAC 962
 QY 338 LysArgGluIleLeuGluLysValGlyLysGlyLysArgGluLeuValTyLySpGlyLysAsn 357
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 Db 963 AAAGAGAAATCTGAGCGTGTGGATGAGCAGGACTGTGTTATAATTGGAGAAT 1022
 QY 358 SerSerGlyTrpLysGluGlu 365
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 Db 1023 GCCCGAGGATGGAGAAAATGCA 1046
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 US-09-009-913-3
 ; Sequence 3, Application US/09009913
 ; Patent No. 608485
 ; GENERAL INFORMATION:
 ; APPLICANT: AXYS Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Asthma Related Genes
 ; NUMBER OF SEQUENCES: 339
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bozicevic & Reed, LLP
 ; STREET: 285 Hamilton Ave., Suite 200
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/009,913
 ; FILING DATE: 21-JAN-1998
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sherwood, Pamela J
 ; REGISTRATION NUMBER: 36,677
 ; REFERENCE/DOCKET NUMBER: SEQ-4P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-327-3231
 ; TELEFAX: 650-327-3231
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5510 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; MOLECULE TYPE: cDNA
 ; US-09-009-913-3
 Alignment Scores:
 Pred. No.: 1.04e-44 length: 5510
 Score: 555.50 matches: 126
 Percent Similarity: 51.24 conservative: 39
 Best Local Similarity: 39.13% mismatches: 78
 Query Match: 28.06% indels: 79
 DB: 3 gaps: 8
 US-08-978-217-2 (1-371) x US-09-009-913-3 (1-5510)
 QY 59 TripleuGlyGluGlnProGlnPheTpSerLysThrGlnValLeuAspTpIleSerTyr 78
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 Db 356 TCCGATGAAATCTCATCTCAGGTACTGGACCAAGTACAGGTTGGAGTGGCTCCAGC 415
 QY 79 GlyvalGluLysAsnLysTyrAspAlaSerAlaLeuAspPheSerArgCysAspMetAsp 98
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 Db 416 CTCCTGGACACCAACGCTGGATGCCAATTTATCCCTTCAGGTTGGACATCAC 475
 QY 99 GlyAlaThrLeuCysAsnCysAlaLeuGluLeuArgLeuValPheGlyProLeuGly 118
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 Db 476 GCGGACCTCTGACCATGAGTTGGAGGTTACCCGGCGCAGGGACGGGG 535

QY 119 AspGlnLeuHisAlaGlnIleuargAspLeuThr-----SerSerSerSerAspGlu 135
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 Db 536 CAGCTCTCTACAGCAACTTGCACTGTGAAACGCCAGTCAGTAGGAC-- 592
 QY 136 LeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetAlapheGlnGluAlaLeuAsp 155
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 Db 593 -----CTGTCAGTCC----- 604
 QY 156 ProGlyProheAspGlnGlySerProheAlaGlnGluLeuAspaspGlyGlnGln 175
 ||||:
 Db 605 -----ACACIACATCAGTCAGTCAGACTGAC 634
 QY 196 ValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySer 215
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 Db 644 ---TCATCATGAACTCTGGAAAGGAGACTATTATGACCAACTATGTCAG 700
 QY 216 AspValAspIleAspProThrAspGlyIleLeuProSerAspGlyIleArgaspCVs 235
 ||||:
 Db 701 ACAGTAGATTG-----TTGACGCAAACTTC-----TGC 733
 QY 236 LysLys-----GlyAspProLysHisGly 243
 ||:::
 Db 734 CGGGCTCAGATCTCCATGACAACCAACCAGTCACCTCCCTGCGAGTCACCTGATG 793
 QY 244 LysAlaGlyAspArgGlyArgProArglysLeuSerLysGluTyrrTrpAspCysLeuGluGly 263
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 Db 794 AAAAAGGAGGAGACCCCTGGCCAGTGCACACCAA----- 832
 QY 264 LysLysAspSerLysHisAlaProArgGlyThrHisLeuProLysPheIleArgAspIleLeu 283
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 Db 833 -----AAGCACAAACCGAGAACGACTCACTATGGCAATTATCCGGACATTC 883
 QY 284 IleHisProGluLeuAsnGluGlyIleuMetLySTpGluAsnArgHisGluGlyValPhe 303
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 Db 884 TTGAACCCAGACAAACCCAGGATAATAAAATGGAGACCGATCTGGGGCTCTC 943
 QY 304 LysProLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsnSerAsn 323
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 Db 944 AGGTTCTGAAATCAGAGGGCTAGCTGGTAAGAGGAAACAGCAG 1003
 .QY 324 MetTrpTyrGlyIleuSerArgAlaLeuArgTrpTyrIleuSerGluIleuGlu 343
 .|||:
 Db 1004 ATGACTATGAAACTTCAGCGACCTATGAGATTTACTAACAAAGAGAACTGGAG 1063
 QY 344 ArgValAlaGlyIleuArgLeuValTyrLysPheGlyLysAsnSerSerGlyTpyLysGlu 363
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 Db 1064 CGTGTGGATGGAGCAAGACTGGATAATAATTGGAGATGCCGAGATGGAGAA 1123
 QY 364 GluGlu 365
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RESULT 4
 US-009-913-4
 ; Sequence 4, Application US/09009913
 ; Patent No. 6087485
 ; GENERAL INFORMATION:
 ; APPLICANT: AMYS Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Asthma Related Genes
 ; NUMBER OF SEQUENCES: 339
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Bozicovic & Reed, LLP
 ; STREET: 285 Hamilton Ave, Suite 200
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/009 913
 FILING DATE: 21-JAN-1998
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sherwood, Pamela J
 REGISTRATION NUMBER: 36,677
 REFERENCE/DOCKET NUMBER: SEQ-4P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-327-3231
 TELEFAX: 650-327-3231
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5667 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLogy: linear
 MOLECULE TYPE: cDNA
 US-09-009-913-4

Alignment Scores:
 Pred. No.: 1.098-44
 Score: 555.50
 Percent Similarity: 51.24%
 Best Local Similarity: 39.13%
 Query Match: 28.06%
 DB: 3

US-08-978-217-2 (1-371) x US-09-009-913-4 (1-5667)

QY 59 TrpIleGlyGluGlnProGlnPheTrpSerLysThrGlnValLeuAspTrpIleSerTyr 78
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 Db 513 TGGCATGAATTCATCCCTCAGTACTGGACCAAGTACCGGGTGGGAGTGGCTCCAGCAC 572
 QY 79 GlyValGluLysAsnLysTyrAspPalserAarAileAspPheserArgCysAspMetAsp 98
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 Db 573 CTCCCTGGACACCAACCAGCTGCTGAGTCAGTATCCCTTCAGAGGTCTGACATCAC 632
 QY 99 GlyAlaThrLeuCysAsnCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuLys 118
 ||||:
 Db 633 GGCAGGACCTCTGAGCTGAGTGTGAGGAGTCACCGGGGGCAGGACGCCGGGG 692
 QY 119 AspGlnLeuHisAlaGlnIleuArgAspLeuThr-----SerSerSerSerAspGlu 135
 ||||:
 Db 693 CAGCTCTCTACAGCAACTTGAGCATGAGCTGAGCTGAGCTGAGTGTGAGTGAC--- 749
 QY 136 LeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetAlaIleGlnGluAlaLeuAsp 155
 ||||:
 Db 750 -----CTGTCAGTCC----- 761
 QY 156 ProGlyProheAspGlnGlySerProheAlaGlnGluLeuAspaspGlyGlnGln 175
 ||||:
 Db 762 -----ACACACAATGTCATGTGCAAGCTGAC 791
 QY 176 AlasSerProTyrHisProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAsp 195
 ||||:
 Db 792 ACTGAGCCT----- 800
 QY 196 ValSerThrAlaGlyIleGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySer 215
 ||||:
 Db 801 ---TCATCATGAAACCTGGAAAGACGAGACTATTATGACCAACTATGGAGC 857
 QY 216 AspValAspIleAspProThrAspGlyLysLeuAspProSeraspGlyPheArgaspCys 235
 ||||:
 Db 858 ACAGTAGATTG-----TTGACGAGCAAACTTC-----TGC 890

QY 236 LysLys-----GlyaspProLysHsGly 243
 ;:::
 Db 891 CGGGCTCAGATCTCCATGACAACCAACAGTCACCTCTCTGTGCAAGTCACCTGTATG 950
 QY 244 LysArgLysArgLysArgProArgLysLeuSerLysGluTyTrpAspCysIleGluGly 263
 Db 951 AAAAGGAGCAGACCCCTGCCAAGTGGCACACCAA----- 989
 QY 264 LysLysSerLysHsAlaProArgLysThrHisLeuTrpGluPhenLeuArgAspIleLeu 283
 Db 990 -----AcGACAACCCGAGGAGGACTCTATGGAAATTCCGCACATCCTC 1040
 QY 284 IleHisProGluLeuAngLugLysLeuMetLysTrpGluAsnarginHsGluGlyValPhe 303
 ;:::
 Db 1041 TTGAAACCCAGAACAGAACCCAGATATAATGCGAACAGCCGACTGAGGCGCTTC 1100
 QY 304 LysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsnSerAsn 323
 ;:::
 Db 1101 AGGTTCTTGAAATCAGGCACTGGCTAGCTAGGCTAAAGAGAACACAGCAG 1160
 QY 324 MetThrTyRgluLysLeuSerArgAlaMetArgTyRtyRlysArgLysLysLysAsnSerAsn 343
 ;:::
 Db 1161 ATGACCTATGAAAGCTCAGCCGAGCTATGAGATTAATCTACAAACGAAACTCTGAG 1220
 QY 344 ArgValAspGlyArgLysLeuValTyRlysPheGlyLysAsnSerSerGlyTrpLysGlu 363
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 Db 1221 CCTGTGCGATGGACGAGACTGCTGATATAATTGGAAAGATGCCCGAGGAGGAGAA 1280
 QY 364 GluGlu 365
 Db 1281 AATGAA 1286

RESULT 5
 US-09-020-956-44/c
 ; Sequence No. 6261562
 . GENERAL INFORMATION:
 . APPLICANT: Xu, Jianchun
 . TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR NUMBER OF SEQUENCES: 178
 . CORRESPONDENCE ADDRESS:
 . ADDRESSEE: SEED and BERRY LLP
 . STREET: 6300 Columbia Center, 701 Fifth Avenue
 . CITY: Seattle
 . STATE: WA
 . COUNTRY: USA
 . ZIP: 98104
 . COMPUTER READABLE FORM:
 . COMPUTER TYPE: floppy disk
 . COMPUTER: IBM PC compatible
 . OPERATING SYSTEM: PC-DOS/MS-DOS
 . SOFTWARE: PATENT Release #1.0, Version #1.30
 . CURRENT APPLICATION DATA:
 . APPLICATION NUMBER: US/09/020, 956
 . FILING DATE: 09-FEB-1998
 . ATTORNEY/AGENT INFORMATION:
 . NAME: Maki, David J.
 . REGISTRATION NUMBER: 31,392
 . REFERENCE/DOCKET NUMBER: 210121.427C2
 . TELECOMMUNICATION INFORMATION:
 . TELEPHONE: (206) 622-4900
 . TELEFAX: (206) 682-6031
 . INFORMATION FOR SEQ ID NO: 44:
 . SEQUENCE CHARACTERISTICS:
 . LENGTH: 852 base pairs
 . TYPE: nucleic acid
 . STRANDEDNESS: single
 . TOPOLOGY: linear
 . MOLECULE TYPE: cDNA
 . ORIGINAL SOURCE:

US-09-020-956-44
 ; ORGANISM: Homo sapiens
 ; US-09-020-956-44
 Alignment Scores: 2.29e-42
 Pred. No.: 519.50
 Score: 50.97%
 Percent Similarity: 39.03%
 Best Local Similarity: 26.24%
 Query Match: 4
 DB: Gaps: 8

US-09-978-217-2 (1-371) x US-09-020-956-44 (1-852)
 QY 71 GlnValLeuAspTriPileSerTyrgInvalGluLysAsnLysTyrasPleAsnValIle 90
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 Db 850 CAGGTGCGGAGTGGCTCACCTCACCTGCACACCAACGCTGATGCCATATGTC 791
 QY 91 AspPheSerSerArgCysAspMetAspGlyAlaThrLeuGluGlyCysAsnCysAlaLeuGluGluLeu 110
 ;:::
 Db 790 CCTTCCANGAGCTCGACATCACCGGAGGACCTTGAGCATGTTGAGGTC 731
 QY 111 ArgLeuValPheGlyProLysLysAspGlnLeuHsAlaGinLeuLysLeuThr--- 129
 ;:::
 Db 730 ACCGGCGCGGCGGAGGAGCGGGCANCCTCTACGAACTGTGAGCATCTGAAGTGG 671
 QY 130 ---- SerSerSerSerAspGluLeuSerTriPileLeuGluLysAspGly 147
 ;:::
 Db 670 AACGGCCAGTCGAGTAGTGAC----- 650
 QY 148 MetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
 ;:::
 Db 649 --CTGTCACGCTC----- 632
 QY 168 GluLeuLeuAspAspGlyPheGlnGluAlaSerProTyRHisProGlySerCysGlyAlaGly 187
 ;:::
 Db 631 AATGTCATGTCAGACTCC----- 599
 QY 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSer 207
 ;:::
 Db 598 -----TCCATCATORACACCTGGAAAGAGNAGAACTAT 566
 QY 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
 ;:::
 Db 565 TATATGACACCAACTGGTGACAGTAGTTG----TGGACAGCAACTTC 512
 QY 228 ProSerAspGlyPheAspGlyPheAspGlyLysLys----- 237
 ;:::
 Db 511 -----TGCCTGGCTGCACTCTCCATGACAACCAACGCTACCTT 473
 QY 238 -----GlyAspProLysHsGlyLysArgLysArgProArgLysLeuSerLys 255
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 Db 472 CCTGTCAGACTCACCTGATATGAAAAGGCAAGACCCCTGCCAAGTCACACC 413
 QY 256 GluTyRtrpAspCysLeuGluGlyLysLysSerLysHsAlaProArgLysThrIleu 275
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 Db 412 AA-----AAGCACAAACCGAGAGGGCTACTA 383
 QY 276 TrpGluPhenLeuArgAspIleHisProGluLeuAsnGluLysLeuMetLysTrp 295
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 Db 382 TGGAAATCTCGGACATCTCTGACCTGACATTATAATAGG 323
 QY 296 GluAsnarginHsGluGlyValPhenLysPheLeuArgSerGluAlaValAlaGlnLeuTrp 315
 ;:::
 Db 322 GAGACCGATCGAGGGCTCTCAAGTCTGAACTCAGGGCACTGGCTCAGCTATGG 263
 QY 316 GlyGlnLysLysLysAsnSerSerAsnMetThrTyRGlutLysLeuSerArgAlaMetArgTyR 335
 ;:::
 Db 262 GCTAAAGAAGAACACAGCGCATACCTTGAAAGCTCGCCAGCTATGAGAT 203
 QY 336 TyrTyryLysArgLysLysLeuLysArgValAspGlyArgLysLeuValTyRlysPheGly 355
 ;:::
 Db 202 TCTTACAAAGGAAATCTGAGCGCTGTGGATGGAGGAACTGGTATATAATTGG 143

Qy 356 LysSerSerSerGlyTyrpysgluGlugluGlu 365
Db 142 AAGATGCCGAGGATGGAGAAATGAA 113

RESULT 6

Sequence 44 Application US/09030607
Patent No. 622245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-44

Alignment Scores:
Pred. No.: 2.29e-42
Score: 519.50
Percent Similarity: 50.97%
Best Local Similarity: 39.03%
Query Match: 26.24%
DB: 4 Gaps: 8

Length: 852
Matches: 121
Conservative: 37
Mismatches: 73
Indels: 79

US-08-978-217-2 (1-371) x US-09-030-607-44 (1-852)

Qy 71 GlnValLeuAspTriPheSerTyrGlnValGluysAsnlysTyrAspAlaSerAlaLle 90
Db 850 CAGGTGTTGGAGTCGCCTCACCTCTGACACCAACCGAGCTGATGCCAATGTATC 791

Qy 91 AspPheSerArgCysAspMetAspGlyAlaThrIleCysAlaLeuGluGluLeu 110
Db 790 CCTTCCANGAGTGCACATCAACGGCGGACCTTGCGACATGAGTTCGAGGTC 731

Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr-- 129
Db 730 ACCGGGCCAGGGCAGGGGGCANCCTCTCAGCACTTCAGCTGAGTC 671

Qy 130 -----SerSerSerAspGluLeuSerTriPheLeuLeuGluIleGlyAspGly 147
Db 670 AACGGGCCAGGGCAGTAGTGC 650

RESULT 7

US-09-605-785-44/C
Sequence 44, Application US/09605785
Parent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocke, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fander, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, AlJjun
APPLICANT: Skeky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16

Qy 148 MetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnDlySerProPheAlaGln 167
Db 649 --CTGTTCCAGTC--.....ACACAC 632

Qy 168 GluLeuLeuAspaspGlyGlnGlnAlaSerProTyrisProGlySerCysGlyAlaGly 187
Db 631 ATGTCATGTCGAAGACTGAACTGAGCC----- 599

Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerSerGlySer 207
Db 598 -----TCCATCATGAACTGCAACCTGGAAAGACINAAGACT 566

Qy 208 HisSerSerAspSerGlySerAspAlaPheLeuAspProThrAspGlySerLeuIle 227
Db 565 TATATGACACAACTATGGTAGCAGCACTAGATTG----TTGGACAGCAACCTTC 512

Qy 228 ProSerAspGlyPheArgAspGlySerLys----- 237

Db 511 -----TSCGGGGTCAGATCTCCATGACAACCAACCACTCACCT 473

Qy 238 -----GlyAspProLyshisGlyLysArgLysArgLyshisArgLysLeuSerLys 255

Db 472 CTCTTGCGAGTCGACCTGATGAAAGAGGCAAGCCCCCTGCCAACGCAACCCT 413

Qy 256 GlutYrrTrpAspCysLeuGluGlyLysSerLysSerLysAlaProArgGlyThrIle 275
Db 412 AAA-----.....ARGCAACCCGAGGGACTCACTA 393

Qy 276 TrpGluPheLeuArgAspLeuLeuLeuHisProGluLysAspGluGlyLysLeuSerLys 295
Db 382 TGGGATTCTCCGGACATCCTCTGACCTGAACTGAACTGAACTGAACTGAACTG 323

Qy 296 GluAsnArgGlyGluGlyValPhelysPheLeuLysSerGluAlaValAlaGlnLeuTrp 315
Db 322 GaAGACCGATCTGAGGGCCTCTGAGGTCTCTGAAATCAGAGCAGTGCTGCTATGG 263

Qy 316 GlyGlnLysLysLysAspSerAsnMetThrGlyLysLeuSerAspSerAlaMetArgYr 335
Db 262 GTAAAGAAGGAAACACGCCAGCATGACTATGAAAGCTCCGGACTATGAGAT 203

Qy 336 TyrTyrLysArgGluLeuGluArgValAspGlyLysGlyValArgLeuValTyrLysPhedY 355
Db 202 TACTACAAGAGGAATTCTGAGCGTGAGATGACGAGACTGGTATAATTGG 143

Qy 356 LysSerSerSerGlyTyrpysGluGluGlu 365
Db 142 AAGATGCCGAGGATGGAGAAATGAA 113

CURRENT APPLICATION NUMBER: US/09/605,785
 CURRENT FILING DATE: 2000-06-27
 NUMBER OF SEQ ID NOS: 835
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 44
 LENGTH: 852
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1)..(852)
 OTHER INFORMATION: n = A,T,C or G
 US-09-605-785-44
 Alignment Scores:
 Pred. No.: 2.29e-42 Length: 852
 Score: 519.50 Matches: 121
 Percent Similarity: 50.97% Conservative: 37
 Best Local Similarity: 39.03% Mismatches: 73
 Query Match: 26.24% Indels: 79
 DB: 4 Gaps: 8
 US-08-978-217-2 (1-371) x US-09-605-785-44 (1-852)
 Qy 71 GlnValLeuAspTriPheSerTyrGlnValGluLysAsnLysTyrAspAlaSerAlaIle 90
 Db 850 CAGGTCTGGAGTCGCATCACCTCCTGGACACCAACAGCTGATGCCATTGTC 791
 Qy 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnCysAlaLeuGlugIleu 110
 Db 790 CCTTCCANGACTTCGACATCACGGCGAGCACCTTGCGASCATGAGTTGCGAGGTT 731
 Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr-- 129
 Db 730 ACCGGGGCGGAGGGAGGGGGGAGCTCCCTCTACGCAACTTGCGACATGAGTGG 671
 Qy 130 ----SerSerSerAspGluLeuSerTriPheIleGluLeuLeuGluLysAspGly 147
 Db 670 AACGCCAGTGCAGTGCAGTAGTGCAC 650
 Qy 148 MetAlaPheGlnGluAlaLeuAspProDlyProPheAspGlnGlySerProHeAlaGln 167
 Db 649 --CTGTTCCAGTCC-----ACACAC 632
 Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyRHisProGlySerCysGlyAlaGly 187
 Db 631 AATGTCATGTCAGACTGAACTGAGCT----- 599
 Qy 188 AlaProSerProGlySerSerAspSerThrAlaGlyAlaSerArgSerSer 207
 Db 598 -----TCCATCATGACACCTGGAAAGACAGNAACTAT 566
 Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyIleuPhe 227
 Db 565 TTATGACACCAACTATGGTAGCACAGTAGTTG-----TTGACAGCAAACCTTC 512
 Qy 228 ProSerAspGlyPheArgAspCysLysIys----- 237
 Db 511 -----TGCGGGCTCAGATCTCCATGACACCAACAGTCACCT 473
 Qy 238 -----GlyAspProLysHisGlyLysArgGlyAspProAspGlyLeuSerLys 255
 Db 472 CCTGTCGAGAGTCACCTGATATGAAAGAGGACAGCCCCCTGCCAACGCCACC 413
 Qy 256 GluTyrrTrpAspCysLeuGluGlyLysSerLysSerLysAlaProArgGlyThrHsIleu 275
 Db 412 AAA-----AAGACAACCGAGGGACTCACTTA 383
 Qy 276 TrpGluPheIleArgAspIleLeuLeuLeuHisProGluLeuAspGluGlyLeuMetLyTrp 295
 Db 382 TGGGAACTCAACGGGACATCTCTGACGAGCAGAAACCCAGGTTATAAATGG 323
 Qy 296 GluAsnArgHisGluGlyIvaPhelysPhelauArgSerGluAlaValAlaGlnLeuTrp 315

RESULT 8
 US-09-439-313-44/C
 ; Sequence 44, Application US/09439313
 ; Patent No. 6239505
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Harlockier, Susan Louise
 ; APPLICANT: Jiang Yuqui
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121-427C9
 ; CURRENT APPLICATION NUMBER: US/09/439,313
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 575
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 44
 ; LENGTH: 852
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(852)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-439-313-44
 Alignment Scores:
 Pred. No.: 2.29e-42 Length: 852
 Score: 519.50 Matches: 121
 Percent Similarity: 50.97% Conservative: 37
 Best Local Similarity: 39.03% Mismatches: 73
 Query Match: 26.24% Indels: 79
 DB: 4 Gaps: 8
 US-08-978-217-2 (1-371) x US-09-439-313-44 (1-852)
 Qy 71 GlnValLeuAspTriPheSerTyrGlnValGluLysAsnLysTyrAspAlaSerAlaIle 90
 Db 850 CGGTCTGGAGTCGCATCACCTCCTGCAACGACATGCCATTGTC 791
 Qy 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnCysAlaLeuGlugIleu 110
 Db 790 CCTTCCANGACTTCGACATCACGGCGAGCACCTTGCGACGATGTTGCGAGGTC 731
 Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr-- 129
 Db 730 ACCGGGGCGGGAGGGGAGCAGCAGCTCTCTACGCAACTTGCGACATGTCAGTGG 671
 Qy 130 ----SerSerSerAspGluLeuSerTriPheIleGluLeuLeuGluLysAspGly 147
 Db 670 AACGCCAGTGCAGTAGTGCAC----- 650

QY 148 MetAlaPheGlnGluAlaLeuAspProGly-ProPheAspGlnGlySerProHeAlaGln 167
; OTHER INFORMATION: n = A,T,C or G
; US-09-352-616A-44
Db 649 ---CTGTTCCAGTCC-----ACACAC 632
; Sequence 44, Application US/09352616A
; Pred. No.: 2-29e-42 Length: 852
; Score: 519.50 Matches: 121
; Percent Similarity: 50.97% Conservative: 37
; Best Local Similarity: 39.03% Mismatches: 79
; Query Match: 26.24% Index: 79
; DB: 4 Gaps: 8
US-08-978-217-2 (1-371) x US-09-352-616A-44 (11-852)
QY 208 HisSerSerAspSerGlySerAspValSerThrAlaLaglyThrGlyAlaSerArgSerSer 207
; Db 598 -----TCATCATGAAACACTGGAAAGACNAGACTAT 566
; QY 228 ProSerAspGlyPheArgAspCysLysLys-----
; Db 511 -----TGCCGGCTAGATCTCATGACACACCAGTCCT 473
; QY 238 -----GlyAspProLyshGlyLysArgSerValAspProThrAspGlyLysLeuPhe 227
; Db 565 TTATAGGACACCAACTATGCTGAGCACTGATTC 512
; QY 228 ProSerAspGlyPheArgAspCysLysLys-----
; Db 472 CCTGTGCAAGTCACCTGATATGAAAGGCGAACCCCCTCCAGTCAGCTGCAAC 413
; QY 256 GluTy-TrpAspCysLeuGluGlyLysLeuPhe 237
; Db 412 AAA-----
; Db 512 TGGGATTCTCCGCACTCTCTGAACCCAGACAAAGACCAAGGATTATAATG 323
; QY 276 TrpGluPheLeuArgAspIleLeuHisProGluLeuAsnGluLysLeuMetLysTrp 295
; Db 322 GAAGACCGATCTGAGGCGCTCTCAGTCAGTCAGCTGCACTGAGCTATGG 671
; QY 316 GlyGlyLysLysSerAsnMetThrTyrglyLysLeuSerArgAlaMetArgTyr 335
; Db 262 GGTAAAGAAGGAAACACAGCGCATGACCTCTGAAAGCTCAGCCGAGCTAGAT 203
; QY 336 TyrTyrylSargGluIleLeuGluArgValAspGlyArgLeuValTyrLysPheGly 355
; Db 202 TACTACAAGAGAAATTCTGGAGCTGGATGGACGAAAGACTGGTATAATAATTGG 143
; QY 356 LysAsnSerSerGlyTriplcGluGluGlu 365
; Db 142 AAGATATGCCGAGGATGGAGAGAAATGAA 113
RESULT 9
US-09-352-616A-44/C
; Sequence 44, Application US/09352616A
; Patent No. 639527B
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlicker, Susan Louise
; APPLICANT: Jiang, Yugui
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121_42C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: misc_feature
; LOCATION: (1)...(852)

Alignment Scores:
Pred. No.: 2-29e-42 Length: 852
Score: 519.50 Matches: 121
Percent Similarity: 50.97% Conservative: 37
Best Local Similarity: 39.03% Mismatches: 79
Query Match: 26.24% Index: 79
DB: 4 Gaps: 8

QY 71 GluValLeuAspProLeuSerTyrGlyAlaLysAsnLysTyrAspAlaLeu 90
; Db 850 CAGGTGAGGTGCTCCATCACCCCTGACACAAAGCTGGATGCAATTGTATC 791
; QY 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnCysAlaLeuGluGluLeu 110
; Db 730 ACCCGGCCAGGAGGGGGGCAGNCCTCTACAGCACTTGAGCATCTGAGTGG 671
; QY 130 -----SerSerSerAspGluLeuSerTripleGluLeuLeuGluLysAspGly 147
; Db 670 AACGGCAGTCAGTCAGTCAG 650
; QY 148 MetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySerProHeAlaGln 167
; Db 649 ---CTGTTCCAGTCC-----ACACAC 632
; QY 168 GluLeuLeuAspAspGlyGlnGlyAlaSerProTyriHisProGlySerCysGlyAlaGly 187
; Db 598 -----
; Db 631 AAATGTCATTGTCAGTCAGCAACTGAGCT----- 599
; QY 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
; Db 565 TTATAGGACACCAACTATGCTGAGCACTGAGCTGAAAGCTCAGCCGAGCT 512
; QY 228 ProSerAspGlyPheArgAspCysLysLys-----
; Db 511 -----TGCCGGCTAGATCTCATGACACACCAGTCCT 473
; QY 238 -----GlyAspProLyshGlyLysArgSerValAspGlyLysLeuPhe 227
; Db 555 TTATAGGACACCAACTATGCTGAGCACTGAGCTGAAAGCTCAGCCGAGCT 512
; QY 256 GluTy-TrpAspCysLeuGluGlyLysLys-----
; Db 412 AAA-----
; Db 512 TGGGATTCTCCGCACTCTCTGAACCCAGACAAAGACCAAGGATTATAATG 323
; QY 276 TrpGluPheLeuArgAspIleLeuHisProGluLeuAsnGluLysLeuMetLysTrp 295
; Db 322 GAAGACCGATCTGAGGCGCTCTCAGTCAGTCAGTCAGCTGCACTGAGCTATGG 671
; QY 316 GlyGlyLysLysSerAsnMetThrTyrglyLysLeuSerArgAlaMetArgTyr 335
; Db 262 GGTAAAGAAGGAAACACAGCGCATGACCTCTGAAAGCTCAGCCGAGCT 203
; QY 336 TyrTyrylSargGluIleLeuGluArgValAspGlyArgLeuValTyrLysPheGly 355
; Db 202 TACTACAAGAGAAATTCTGGAGCTGGATGGACGAAAGACTGGTATAATAATTGG 143

Qy 356 LysAsnSerSerGlyTirPlysGluGlu 365
Db |||||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 142 AAGAATGCCGAGGATGGAGAAATGAA 113

RESULT 10
US-09-232-149A-44C
Sequence 44, application US/09232149A
; PATENT NO. 6455611
; GENERAL INFORMATION:
; APPLICANT: XU, Jiangchun
; APPLICANT: Billon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121-427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: misc_feature
; LOCATION: (1..(852))
; OTHER INFORMATION: n = A,T,C or G
; US-09-232-149A-44

Alignment Scores:
pred. NO.: 2.29e-42
Score: 5.19.50
Percent Similarity: 50.97%
Best Local Similarity: 39.03%
Query Match: 26.24%
DB: 4 Gang: 8

Length: 852
Matches: 121
Conservative: 37
Mismatches: 73
Indels: 79

US-08-978-217-2 (1-371) x US-09-232-149A-44 (1-852)

Qy 71 GlnValLeuAspTriPileSerTyrglnValGluLysnLysTyrAspAlaSerAlaLe 90
Db 850 CAGGTGCTGGATGCTCATCACCTCTGGACACCTTCAGGATGTTGGAGGATTC 791

Qy 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnCysAlaLeuGluLeu 110
Db 790 CCTTCCANGAGTCGACATCACGCGAGACCTTCAGGATGTTGGAGGATTC 731

Qy 111 ArgLeuValPheCylProLeuGlyAspGlnLeuIleAlaGlnLeuArgAspLeuThr-- 129
Db 730 ACCGGGGGGAGGACGGCCANCTCTAACAGCAACTTGACATCTGAAGTGG 671

Qy 130 ---SerSerSerSerAspGluLeuSerTriPileIleGluLeuLeuGluLysAspGly 147
Db 670 AACGGGGCAGTCGAGTGCAC 650

Qy 148 MetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
Db 649 --CTGTCAGCC---ACACAC 632

Qy 168 GluLeuLysAspAspGlyGlyGlnGlnAlaSerProTyRhiProLySerCysGlyAlaGly 187
Db 631 AATGTCATGTCAAGACTGACAACTGACCT 599

Qy 188 AlaProSerProLySerSerAspValSerThrAlaGlyThrdlyAlaSerArgSerSer 207
Db 598 ---TCCATCATGAACTGCAACCTGGAAAGACNAGACTAT 566

Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
Db 565 TTATATGACCACTATGGTAGCAAGATGATTG---TTGGACAGCAACTRTC 512

Qy 228 ProSerAspGlyPheAspAspCysLysLys----- 237

Db 511 -----TGCCTGGCTGAGATCTCCATGACACACACAGTCACCTT 473
Qy 238 -----GlyAspProLyShiSglyLysArgLysAsgGlyArgProArgLysLeu 255
Db 472 CCTGTCAGAGTCACCTGATATGAAAGGCAAGACCCCCCTCCAGTGCACACC 413
Qy 256 GluTyrrrpaspCysLeuGluGlyLysSerLysHisAlaPrArgGlyThrHisLeu 275
Db 412 AAA-----AAGCACACCCGAGGGCTACTTA 383

Qy 276 TrpGluPhelleArgAspIleLeuHisProGluLeuAspGluGlyLeuMetLysTrp 295
Db 382 TCGGAATTTCATCGCCACATCCTCTGAAACCCAGACAGCAACCCAGATTATAAATGG 323

Qy 296 GluAsnArgHisGluGlyValPhelysPhelLeuIargSerGluAlaValAlaGlnIeuTrp 315
Db 322 GAGACCGATCTGAGGGCTCTCAGGTTCTGAAATCAGGCACTGGCTCAGCTTGG 263

Qy 316 GlyGlnLysLysLysAsnSerAsnMetThrArgLysLeuSerArgLametArgTyr 335
Db 262 GCTAAAGAAGAACAGACAGCAGCTGACCTATGAAAGCTCAGCCAGCTATGAGAT 203

Qy 336 TyrTyrLysAspGluIleLeuGluAspGlyArgArgLeuValTyrLysPheGly 355
Db 202 TACTACAAGGAAATCTGGAGCGCGTGGATGGACGAAGACTGGTATAATTGG 143

Qy 356 LysAsnSerSerGlyTirPlysGluGlu 365
Db 142 AAGAATGCCGAGGATGGAGGAAATGAA 113

RESULT 11
US-09-009-913-338
; Sequence No. 338, Application US/0909913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: AXYS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE DOCKET NUMBER: SEQ-4-P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-2311
; TELEX:
; INFORMATION FOR SEQ ID NO: 338:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

NAME/KEY: Coding Sequence ;
 LOCATION: 1..848 ;
 OTHER INFORMATION: US-09-009-913-338

Alignment Scores:		Length:		Score:			
Preド. No.:	4.15e-39	848		Percent Similarity:	486.50		
				Conservative:	109		
				Mismatches:	51.53%		
Best Local Similarity:	36.95%			Indels:	43		
Query Match:	24.57%			Gaps:	88		
DB:	3				55		
US-08-978-217-2 (1-371) x US-09-009-913-338 (1-848)							
QY	57 AlaserTrpLeuGlyGlugLnnProGlnPheTrpSerLySthrGlnValLeuAspTrpIle	76		QY	77 SerTyrgInvalGluLysAsnLyStyAspAlaSerAlaLeuAspPheSerArgCysAsp	96	
Db	118 AGCCAGTCGCGATGAATCCACCTCTAGTCACTGGAAATGGCTG	177		Db	178 CAGCACCTCTGACACCAACCAGCTAGACGGCTAGTCGAC	237	
QY	97 MetAspGlyAlaThrLeuCysCysAlaLeuGluLeuArgLeuValPheGlyPro	116		QY	98 AspGluLeuSerTrpIleLeuGluLeuGluLysAspGlyMetAlaPheGlnGua	153	
Db	238 ATTAGCGGAGAACACCTGTGCAGCATGAGTCAGCAGGAGTCACGAGGGAGCAGCTCA	297		QY	117 LeuGlyAspGlnLeuHisAlaGlnLeuArgLeuAspLeuThr	133	
QY	174 GlnglnAlaSerProTyRHisProGlySerCysGlyAlaGlyAlaProSerProGlySer	193		Db	298 GCTGGGAGCTCTCACGCAACCTACGCTCTCAAGTGAAACGCCATGCACTG	357	
Db	358 GACCTTTCACTCCGACACATGCTGATGTCAG	402		QY	134 AspGluLeuSerTrpIleLeuGluLeuGluLysAspGlyMetAlaPheGlnGua	153	
QY	154 LeuAspProGlyProLeuAspGlnGlySerProHealaGlnGluLeuLeuAspGly	173		Db	403 ACCGATCCT-----TCCATCATGACACATG	429	
Db	490 AAGACTTCTCGCGGGCTCAGATCTCCATGACACCTCCAGTCACCTCAGTGCAG	549		QY	174 GlnglnAlaSerProTyRHisProGlySerCysGlyAlaGlyAlaProSerProGlySer	193	
Db	430 AAAGAAGAAACTATCTCTATGATCCAGCTATGGACAGTAGATCTGTGGACAGT	489		Db	430 AAAGAAGAAACTATCTCTATGATCCAGCTATGGACAGTAGATCTGTGGACAGT	489	
QY	194 SerAspAlaSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerAspArgIle	213		QY	194 SerAspAlaSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerAspArgIle	213	
Db	550 TCACCTGATG-----561	561		Db	550 TCACCTGATG-----561	561	
QY	214 GlySerAspValAspLeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArg	233		QY	234 AspCysLysLysGlyAbpProLyBHiGlyLyBargLysArgGlyArgProLyGlyLeu	253	
Db	562 -----AlaGAGGCAAGCACCT-----582	582		Db	562 -----AlaGAGGCAAGCACCT-----582	582	
QY	254 SerLysGluTyTrpAspCysLeuGluGlyLysSerLysBisAlaProArgGlyThr	273		QY	274 HisLeuTrpGluPhelLeArgAspIleLeuLehIsProGluLeuLeuGluGlyLeuMet	293	
Db	583 -----GtaAGGRCACACCAAAGACACAACGAGGACT-----621	621		Db	622 CACTATGGGACTTCATCCGAGACATTCTCTGAGGCCAAAGACAGAACCCAGGCTCATC	681	
QY	294 LysTrpGluAsnArgHiGluGlyValPhelLepheLeuAspSerGluIalaValAlaGin	313		QY	79 GlnValGluLysAsnLyStyAspAlaSerAlaLeuAspPheSerArgCysAspMetAsp	98	
Db	682 AATGGGAAACGCCGTCGGAGGCATCTCAGTCTGAGTCAGACAGCTGGCTCAG	741		Db	266 TCTGCGGACGAGTACAGTGGACACAAATGCACTCTCTGCACTTCACATCAGT	325	
QY	314 LeutTrpGlyGlyLysLysLysAsnSerAsnMetThrTrpGluGlyLeuSerArgAlaMet	333		QY	99 GlyAlaThrLeuCysCysCysAlaLeuGluLeuArgLeuValPheGlyProLeuGly	118	
Db	742 CTGTTGGGGAAAGAAAATAACAGTGACATAGCACTAGGAGCTGACGCTGAGCTG	801		Db	326 GGCTGCGAGCTGCGACATGACACAGGAGGTTGTCGAGGACCTGGCTCTCGGC	385	
QY	334 ArgTYRTTYTYLYSAQGQuileLeuQuargValAspGlyArg 348			QY	119 AspGlnLeuHisAlaGlnLeuArgLeuAspLeuSerSerSerAspGluLeuSerTrp	138	
Db	386 GAGTACCTGTACTCTCATCTCCGAGAACATCCGCA			Db	386 GAGTACCTGTACTCTCATCTCCGAGAACATCCGCA	421	
QY	139 IleLeuGluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyPro	158					

Db 421 ----- 421
 Qy 159 PheAspGlnGlySerProPheAlaGlnLeuLeuAspAspGlySerGlnAlaSerPro 178
 Db 422 -----CAGGTACTCTTTTAATGACCGTGAAGCAAGGCCACCATCAAAGAC 475
 Qy 179 TyrHisProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThr 198
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 476 TATGCTGATTCCGACTGC-----TTGAAACA 502
 Qy 199 AlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAsp 218
 ::| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 503 AGTGGCCTC--AAAAGTCAGACTGTCACAGT----- 532
 Qy 219 LeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysGly 238
 Db 532 ----- 532
 Qy 239 AppProLySisGlyLysArgLysArgLysArgProArgLysLeuSerLysGluTyTrp 258
 Db 532 ----- 532
 Qy 259 AppCysLeuGluGlyLysSerLysSerLysAlaProArgGlyThrHisLeuTrpGluPhe 278
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 533 -----CATAGTAGAACAAAGCTCCAAGTCTCATCTATGGAAATT 574
 Qy 279 TieArgAspIleLeuIleHisProGluLeuAsnGlyLeuMetLysTrpGluAspArg 298
 ::| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 575 GRACGAGCTGCTCTCTCTCTGAGAAACTGTGCGATCTGGATGGAGATGG 634
 Qy 299 HisGluGlyValPhenylsPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlyLys 318
 ::| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 635 GRACAGGAATTCTTCTCGGGTGTAAATGGAAAGCCTGGCAAAAGTGCGAACAGG 694
 Qy 319 LysLysIsoleSerAsnMetThrThrTyrGluLysLeuSerArgAlaMetAlaGlyTyTyTyTyLys 338
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 695 AACGAAATAATGACGAGATGACGTTGAAAGTGGAGAGCCCTGAGATACTATCAA 754
 Qy 339 ArgGluIleLeuIleGluArgValAspGlyLysArgGluLeuValTyrLysPheGlyLysSer 358
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 755 ACAGGAATTGGAGCGGTGAC--CGAACGTTAGTGTACAAATTGGAAAATGCA 811
 Qy 359 SerGlyTrpLysGluGluVal 366
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 812 CACGGTGTGCAAGGAAAGCAAGCTA 835

RESULT 13

US-09-009-913-6
 Sequence 6, Application US/09009913
 Patent No. 608485

GENERAL INFORMATION:

APPLICANT: Axxys Pharmaceuticals, Inc.

TITLE OF INVENTION: Asthma Related Genes

NUMBER OF SEQUENCES: 339

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP

STREET: 285 Hamilton Ave., Suite 200

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastaSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,913

FILING DATE: 21-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J

REGISTRATION NUMBER: 36,677

REFERENCE/DOCKET NUMBER: SEQ-4P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-327-3231

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 2428 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-009-913-6

Alignment Scores:

DB:	Score:	Length:	Matches:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Score:	Length:	Matches:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Score:	Length:	Matches:	Percent Similarity:	Best Local Similarity:	Query Match:		
	4.74e-32	2428	90	42.00	45.45%	29.22%		4.74e-32	2428	90	42.00	45.45%	29.22%		4.74e-32	2428	90	42.00	45.45%	29.22%		
			50							50								50				
			70							70								70				
			98							98								98				
			5							5								5				
			3							3								3				
			Gaps:							Gaps:								Gaps:				

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Qy 59 TripleGlyGluGlnProGlnPheProSerLysThrGlnValLeuAspTpLeSerTyr 78
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 354 TGGACATCAGTCACCTGAACTGACTGAGCTAGGCCATGTGGATGGCTCCAGTTC 413
 Qy 79 GluValGluLysAsnLysTyrAspPheSerAlaSerAlaAspPheSerArgCysAspMetAsp 98
 ::| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 414 TGTGCGGACGACGATCACAGTGGACACCAATTGATCCTCTGCAACTCACATGAT 473
 Qy 99 GlyAlaThrLeuCysAsnCysAlaLeuGluGluLeuArgLeuValPheGlyProGly 118
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 474 GGCCTGCGAGCTGCGAGCATGAGCACAGGAGKGTCTCGAGGCAGCTGGCTCTCGCGC 533
 Qy 119 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerSerAspGluLeuSerTrp 138
 ::| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 534 GAGTACCTGACTTCATCCTCCAGAACATCCGCACA----- 569
 Qy 139 TieIleGluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyPro 158
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 569 ----- 569
 Qy 159 PheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlySerGlnAlaSerPro 178
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 570 -----CAGGTACTCTTCTTTAATGACCGTGAAGCAAGGCCACCATCAAAGAC 623
 Qy 179 TyrHisProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThr 198
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 624 TATGCTGATTCCGACTGC-----TTGAAACA 650
 Qy 199 AlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAsp 218
 ::| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 651 AGTGGCCTC--AAAAGTCAGACTGTCACGT----- 680
 Qy 219 LeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysGly 238
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 680 ----- 680
 Qy 239 AppProLySisGlyLysArgLysArgProArgLysLeuSerLysGluTyTrp 258
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 681 -----CATAGTAGAACACCTCCAAGTCTCATCTGAGGAAATT 722
 Qy 279 TieArgAspIleLeuHisProGluLeuAsnGlyLysLeuMetLysTrpGluAsnArg 298

NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS: 9
 ADDRESS: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/368, 281
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Baumeister, Kirk
 REGISTRATION NUMBER: 33, 833
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5096
 TELEFAX: 610-270-5030
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2975 base pairs
 STRANDEDNESS: double
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA
 8-368-281-1

Environment Scores:			
I. No.:	1.41e-14	Length:	
e-value:	246.50	Matches:	
Local Similarity:	40.43%	Conservative:	
Y Match:	12.45%	Mismatches:	
	1	Inels:	
		Gaps:	

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139	IleIleGluLeuLeuLeuGluLySaspGlyMetAlaPheGlnGluI	Length:	
::: :::	:	Matches:	
1	GTCGCTGACTGTGCTCGTCTGCAGGGCCTGCTGCTCCGCCG	Conservative:	
159	PheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGly	Mismatches:	
61	CTG-----CGCCGCGTCACGGCTGAACTGCAATGAA	Inels:	
179	-----TyrIlePr	Gaps:	
112	CGGCGATAAACATGGCGACGCTCTGCTGAGGGACCCACGAACCC		
187	GlyAlaProSerProGlySerSerAspSerValSerThr-----		
160	GGATCTGTCTCATCGGGCCGTTGGAGCATCAGTCACAGCACTTA		
199	-----AlaLysLyThrGlyAlaSer		
220	TAAGACAATTGAAAGCTGTCGTAAGGCCCTGTCTCATGGATCTC		
205	-----ArgSer		
280	TTCAGAAGATGCTCTGAATTCTATCCATGCTGCTATGAGCCAGATG		
212	SerGlyGly-SerAspValAspIleAspProThrAspGlyLysSer		
340	AGTGGAGGTGTCAGTGAAGAGTGACCCATGATACCTCTTC		
230	-AspGlyLpheArgAspCysLysLys		
400	AGATAGCCATGAAACCAATGCAAGAAAAGATGGCGCTAAAC		

Search completed: March 15, 2003, 23:32:40
Job time : 94.0238 secs

